

RL Gene 234:71-79(1999).  
 DR EMBL: AB019623; BAA7351.1; -  
 DR InterPro: IPR001296; Glycosyl-transf.1.  
 DR InterPro: IPR000794; Ketoacyl-synt.  
 DR Pfam: PF00534; Glycosyl-transf.1; 1.  
 DR PROSITE: PS00606; B\_KETOACYL\_SYNTHASE; UNKNOWN\_1.  
 KW Glycosyltransferase; Transferase.  
 SO SEQUENCE 605 AA; 66345 MW; 60A81627678722B CRC64;

Query Match 62.8%; Score 2037.5; DB 10; Length 605;  
 Best Local Similarity 63.7%; Pred. No. 1.6e-148;  
 Matches 381; Conservative 85; Mismatches 113; Indels 19; Gaps 6;

28 GLAFQIRIPYLSNASTFEGLRSN---QMSRPMQCAKATTRQYRKGIQHASRRPSV 83  
 17 GIDFRFR-----AGFGVRRSPADAPLGMRTTGASAPRQQRKAKHGRTRCLSM 68  
 84 IC-----ASGMNLIYAALVAPWSTGTGLGVLGGLPMAAKGHRVMTIARHDOYKDW 139  
 69 VVRATGSGMNLVFGAEMAPWSTGTGLGVLGGLPMAANGHRVMTISPRYDOYKDW 128  
 140 DPAVEVELKVDRIETVFFHCYKRGVDVDFVDPHLEFLEKYGKGTGKTYGPTRTYED 129  
 129 DTSVSEIKVADEYERVRYFHCYKRGVDVDFVDPHLEFLEKYGKGTGKTYGPTRTYED 188  
 200 NQRLRCLLCLATLETPRVLPNNKYNHSGPKGED-LFIANDMHTALPCYKTYGQAHG 258  
 189 NQRLRCLLCLATLETPRVLPNNKYNHSGPKGED-LFIANDMHTALPCYKTYGQAHG 247  
 259 IYKNAKAFCHINIAVQGRFAFEDFSRLNLPDTRKSSDFIDGAKPIKGRKINMMAKI 318  
 248 IYKNAKAFCHINIAVQGRFAFEDFSRLNLPDTRKSSDFIDGAKPIKGRKINMMAKI 307  
 319 IESDRALVSPYPAQELVSGIDKGVLELDNLRKTCIGIINGMDTNMNPSTDKYITANY 378  
 308 LQAKKVLTVSPYPAQELVSGIDKGVLELDNLRKTCIGIINGMDTNMNPSTDKYITANY 367  
 379 DATYMEAKPLNKALQAEVGLPVNSKIPVIAFAGLEQKSGDILAEAIKPF-DOVQ 437  
 368 DVTALBEKALNKALQAEVGLPVNSKIPVIAFAGLEQKSGDILAEAIKPF-DOVQ 427  
 438 VIVATGKKKLEROLALLEDEFPDPRFAHMKFNIPLAGIAGADIVIPSRFPCGLIQ 497  
 428 IVLLGTGKKKLEROLALLEDEFPDPRFAHMKFNIPLAGIAGADIVIPSRFPCGLIQ 487  
 498 LOGMRVGPSCASTGTGLVDTIMEGKTFHMGRLSDVCNVEPADYKVVYTLKRAKVV 547  
 558 GTPAFEEIOMNCAODPSWKGPAKEMEFLLSLGEGSEAGIEEVEAPLAKENAVAP 615  
 548 GTPAFEEIOMNCAODPSWKGPAKEMEFLLSLGEGSEAGIEEVEAPLAKENAVAP 605

## RESULT 14

09F0U6 PRELIMINARY; PRT; 605 AA.

ID 09F0U6  
 AC 09F0U6  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Granule bound starch synthase 1 (EC 2.4.1.21).  
 GN GBSST.  
 OS Triticum aestivum (wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Triticum.  
 OC NCBI\_TaxID=4565;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. CHEYENNE; TISSUE-ENDOSPERM;  
 RA McCue K.E., Hurkman W.J., Tanaka C.K., Anderson O.D.;  
 ST Starch Branching Enzymes Sbe1 and Sbe2 from Wheat (Triticum aestivum

RT cv. Cheyenne); Molecular Characterization, Developmental Expression,  
 RT and Homolog Assignment by Differential PCR.  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF263320; AAC27624.1; -  
 DR InterPro: IPR001296; Glycosyl-transf.1.  
 DR InterPro: IPR000794; Ketoacyl-synt.  
 DR Pfam: PF00534; Glycosyl-transf.1; 1.  
 DR PROSITE: PS00606; B\_KETOACYL\_SYNTHASE; UNKNOWN\_1.  
 KW Glycosyltransferase; Transferase.  
 SO SEQUENCE 605 AA; 66326 MW; 21120D9D6F68B891 CRC64;

Query Match 62.8%; Score 2037.5; DB 10; Length 605;  
 Best Local Similarity 63.7%; Pred. No. 1.6e-148;  
 Matches 381; Conservative 85; Mismatches 113; Indels 19; Gaps 6;

28 GLAFQIRIPYLSNASTFEGLRSN---QMSRPMQCAKATTRQYRKGIQHASRRPSV 83  
 17 GIDFRFR-----AGFGVRRSPADAPLGMRTTGASAPRQQRKAKHGRTRCLSM 68  
 84 IC-----ASGMNLIYAALVAPWSTGTGLGVLGGLPMAAKGHRVMTIARHDOYKDW 139  
 69 VVRATGSGMNLVFGAEMAPWSTGTGLGVLGGLPMAANGHRVMTISPRYDOYKDW 128  
 140 DPAVEVELKVDRIETVFFHCYKRGVDVDFVDPHLEFLEKYGKGTGKTYGPTRTYED 129  
 129 DTSVSEIKVADEYERVRYFHCYKRGVDVDFVDPHLEFLEKYGKGTGKTYGPTRTYED 188  
 200 NQRLRCLLCLATLETPRVLPNNKYNHSGPKGED-LFIANDMHTALPCYKTYGQAHG 258  
 189 NQRLRCLLCLATLETPRVLPNNKYNHSGPKGED-LFIANDMHTALPCYKTYGQAHG 247  
 259 IYKNAKAFCHINIAVQGRFAFEDFSRLNLPDTRKSSDFIDGAKPIKGRKINMMAKI 318  
 248 IYKNAKAFCHINIAVQGRFAFEDFSRLNLPDTRKSSDFIDGAKPIKGRKINMMAKI 307  
 319 IESDRALVSPYPAQELVSGIDKGVLELDNLRKTCIGIINGMDTNMNPSTDKYITANY 378  
 308 LQAKKVLTVSPYPAQELVSGIDKGVLELDNLRKTCIGIINGMDTNMNPSTDKYITANY 367  
 379 DATYMEAKPLNKALQAEVGLPVNSKIPVIAFAGLEQKSGDILAEAIKPF-DOVQ 437  
 368 DVTALBEKALNKALQAEVGLPVNSKIPVIAFAGLEQKSGDILAEAIKPF-DOVQ 427  
 438 VIVATGKKKLEROLALLEDEFPDPRFAHMKFNIPLAGIAGADIVIPSRFPCGLIQ 497  
 428 IVLLGTGKKKLEROLALLEDEFPDPRFAHMKFNIPLAGIAGADIVIPSRFPCGLIQ 487  
 498 LOGMRVGPSCASTGTGLVDTIMEGKTFHMGRLSDVCNVEPADYKVVYTLKRAKVV 547  
 558 GTPAFEEIOMNCAODPSWKGPAKEMEFLLSLGEGSEAGIEEVEAPLAKENAVAP 615  
 548 GTPAFEEIOMNCAODPSWKGPAKEMEFLLSLGEGSEAGIEEVEAPLAKENAVAP 605

## RESULT 15

09SLS6 PRELIMINARY; PRT; 604 AA.

ID 09SLS6  
 AC 09SLS6  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Starch synthase (GBSSI) (EC 2.4.1.21).  
 GN MAY.  
 OS Triticum turgidum subsp. durum (durum wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Triticum.  
 OC NCBI\_TaxID=4567;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC Murali J., Talra T., Ohta D.;